Supplemental Figures
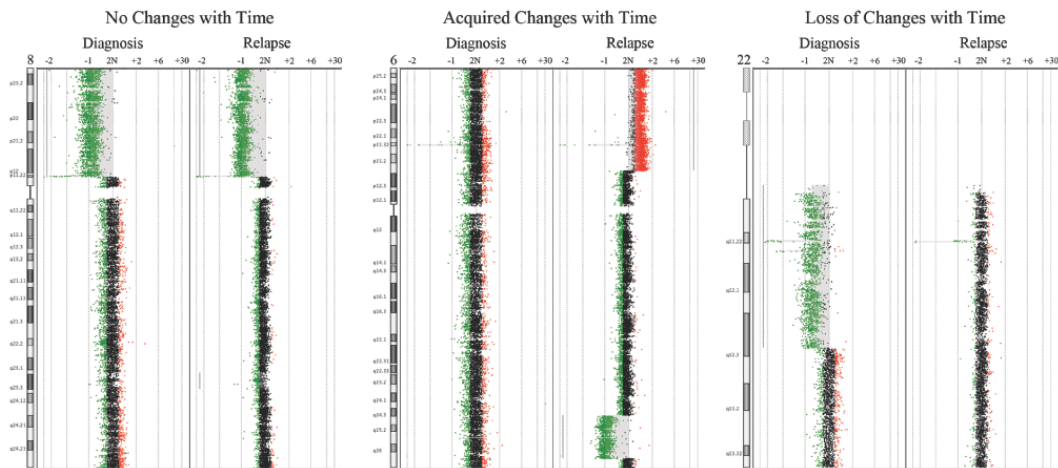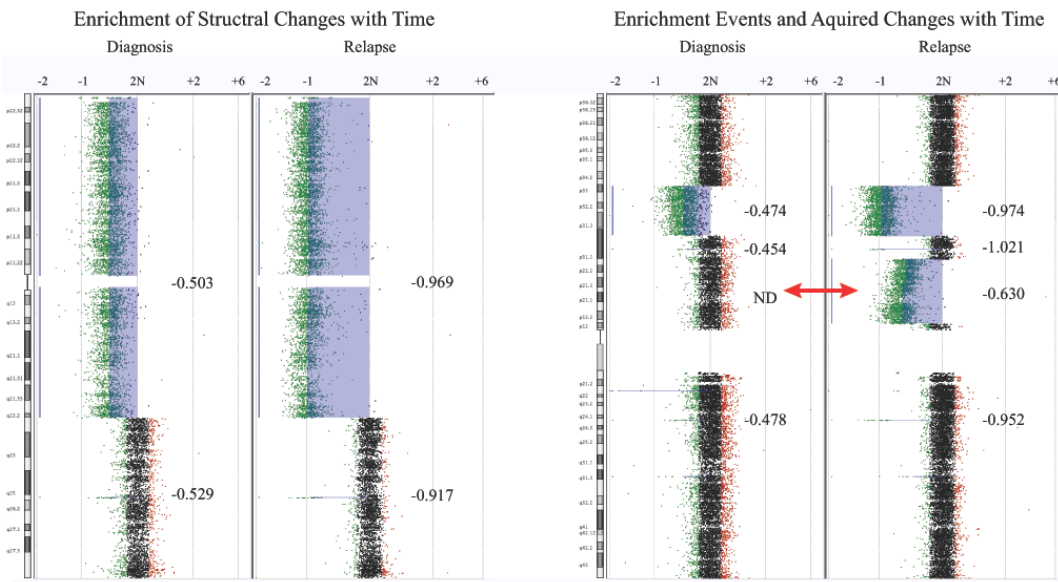
Supplemental Figure 1 – Types of Copy Number Changes Scored


Examples of copy number abnormality (CNA) scoring are shown.

A) Three different temporal CNA phenotypes are shown. In the first panel a chromosome with an identical deletion at diagnosis and relapse is shown. In the second panel an example of acquired abnormalities is shown where two different CNA are present only at relapse. In the third panel an example of a CNA loss is shown where a large deletion present at diagnosis is not detectable at relapse.

B) Because we scored structural changes we did not score enrichment events of abnormalities present at diagnosis. In panel one an example of two co-incident enrichment events is shown and the relative log2 ratios are indicated. In panel two a more complicated scenario is shown where three regions show a similar level of enrichment while a CNA indicated by a red arrow is acquired at relapse.

Supplemental Figure 2 – Chromosome 8 Assay Differentiating Progenitor 1 and 2

A)
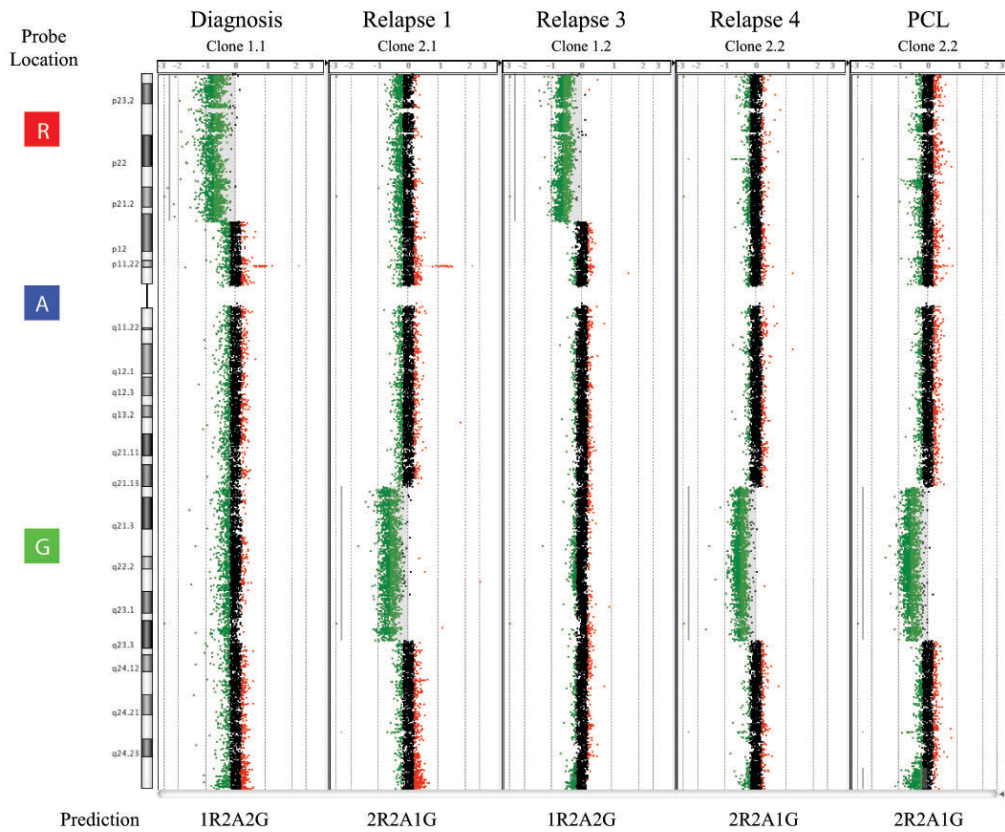
Clone	Phenotype	Diag	Rem	R1	R2	R3	R4 -PC	R4 -LC	PCL-PC	PCL-LC
1.1, 1.2	1R2A2G	84%	100%	31.6%	63.8%	85%	84.2%			
	2R4A4G	2%				1%		1.7%		
Clone 2.1	2R2A1G	12%		67.1%	36.2%	10%				
Clone 2.2	3R3A2G							79.7%	90.0%	84.6%
	4R4A2G							8.5%		
	4R4A3G							1.7%		4.4%
	5R5A3G							1.7%		
Misc	4R3A2G								6.4%	5.5%
	4R2A4G	1%								
	3R2A2G							6.8%	3.7%	5.5%
	2R2A4G					1%				
	1R2A3G						15.8%			
	1R1A2G	1%				2%				
	1R2A1G					1%				
	1R1A1G			1.3%						
Cells		100	22	152	58	100	19	59	109	91

A) The relative position of each FISH probe used to determine the presence or absence of specific chromosomal regions is shown beside the aCGH results.

B) The number of cells counted and the percentage of each phenotype detected by FISH is indicated. The letters indicated under Phenotype correlate with the colors seen in A): red (R), aqua (A) and green (G).

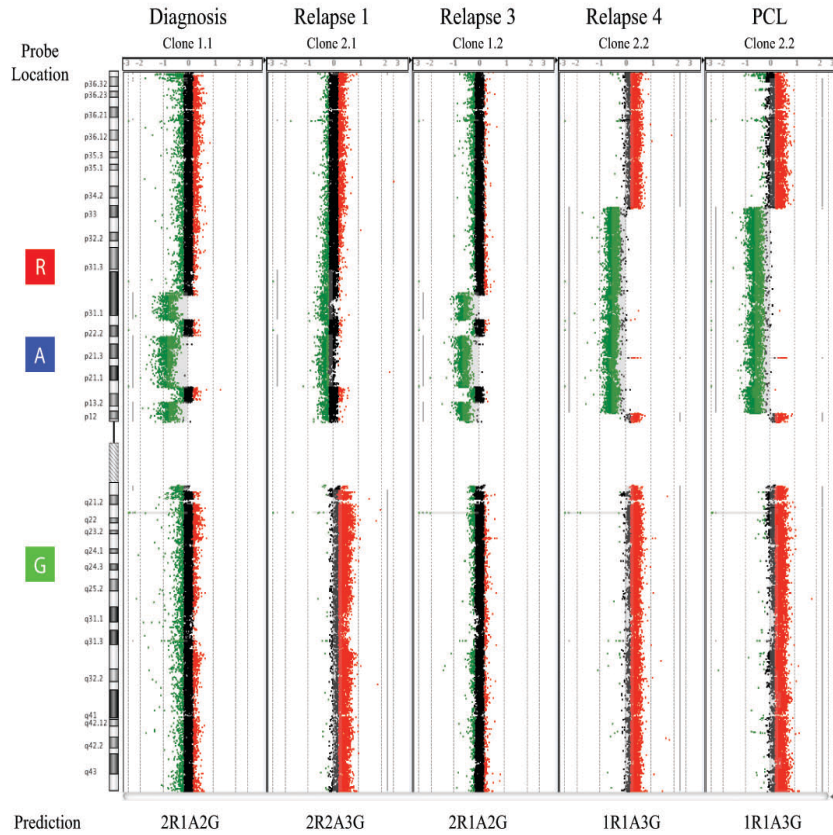Supplemental Figure 3 – Chromosome 6 (1.1 vs 1.2 vs 2.1 vs 2.2)

A)
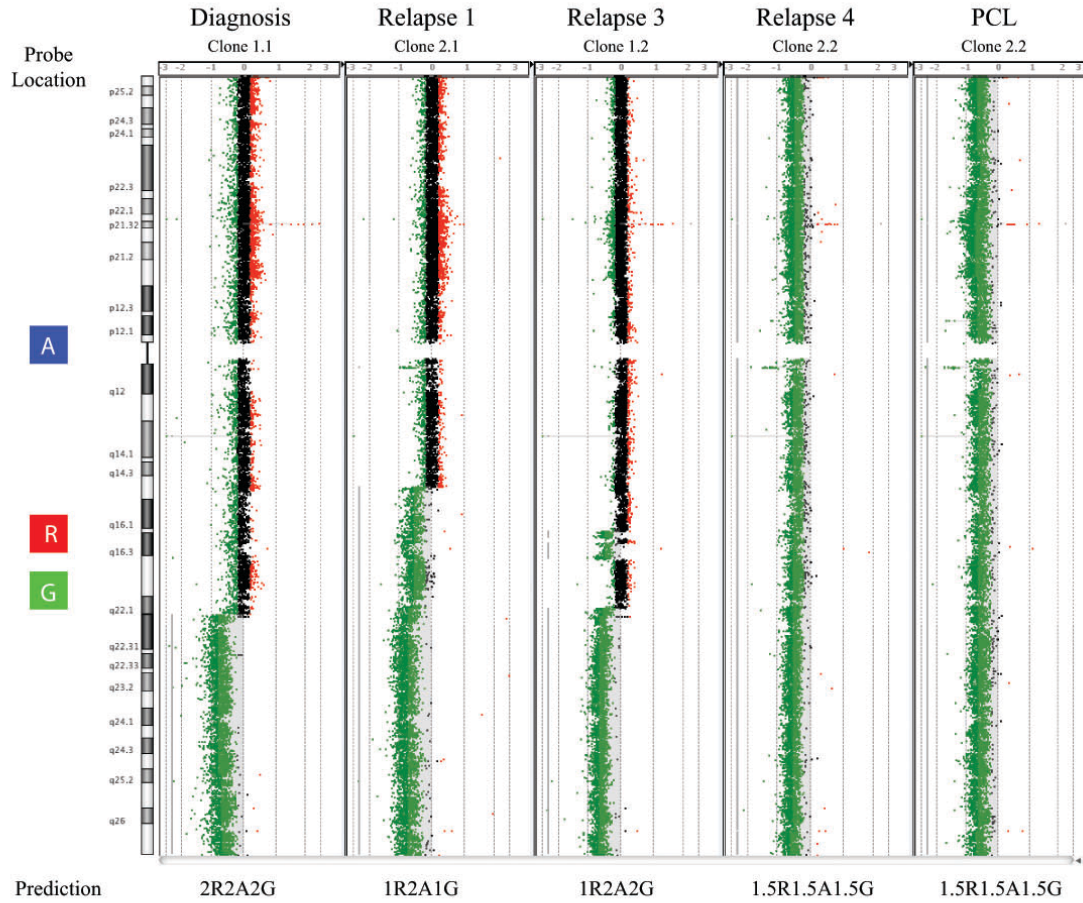
Clone	Phenotype	Diag	Rem	R1	R2	R3	R4 -PC	R4 -LC	PCL-PC	PCL-LC
Clone 1.1	2R2A2G	80.%	67.5%	25%	12%	17%	10.9%			
	4R4A4G	1.0%		0.7%						
Clone 1.2	1R2A2G	12.0%	32.5%	10.8%	82.2%	69%	80.4%			
Clone 2.1	1R2A1G	4.5%		62.8%	5.5%	14%	8.7%			
Clone 2.2	2R2A2G/3							100%	97%	100%
Misc	1R1A2G	0.5%								
	1R1A1G			0.7%	4.1%					
	2R1A2G								2.0%	
	2R2A1G								1.0%	
Cells		200	40	148	73	100	46	100	200	

A) The relative position of each FISH probe is shown beside the aCGH results. See Suppl Figure 2A.

B) The number of cells counted and the percentage of each phenotype shown by FISH. See Suppl Figure 2B.

Supplemental Figure 4 – Chromosome 1 (Progenitor 1 vs 2.1 vs 2.2)

A)

	Diagnosis	Relapse 1	Relapse 3	Relapse 4	PCL
	Clone 1.1	Clone 2.1	Clone 1.2	Clone 2.2	Clone 2.2
Prediction	2R1A2G	2R2A3G	2R1A2G	1R1A3G	1R1A3G

B)

Clone	Phenotype	Diag	Rem	R1	R2	R3	R4 -PC	R4 -LC	PCL-PC	PCL-LC
Clone 1	2R1A2G	84%	94.4%	18.6%	58%	80%	84.6%			
	4R2A4G					12%				
Clone 2.1	2R2A3G			67.4%	8%			9.5%	14.2%	10%
Clone 2.2	1R1A2G			2.3%	26%	2%	3.8%			
	1R1A3G				3%			1.4%		
	2R2A6G						3.8%			
	3R3A5G						3.8%			
	2R2A4G							86.5%	82.5%	86.3%
	2R2A5G							2.7%	3.3%	1.2%
Misc	2R2A2G	12%	2.8%	8.1%	2%	2%				
	2R1A1G	4%		0.6%						
	2R1A3G		2.8%	0.6%	3%	4%	3.8%			
	2R2A1G			0.6%						
	1R2A3G			1.7%						
	2R1A4G									2.5%
Cells			50	36	172	100	50	26	81	120	80

A) The relative position of each FISH probe is shown beside the aCGH results. See Suppl Figure 2A.

B) The number of cells counted and the percentage of each phenotype shown by FISH. See Suppl Figure 2B.

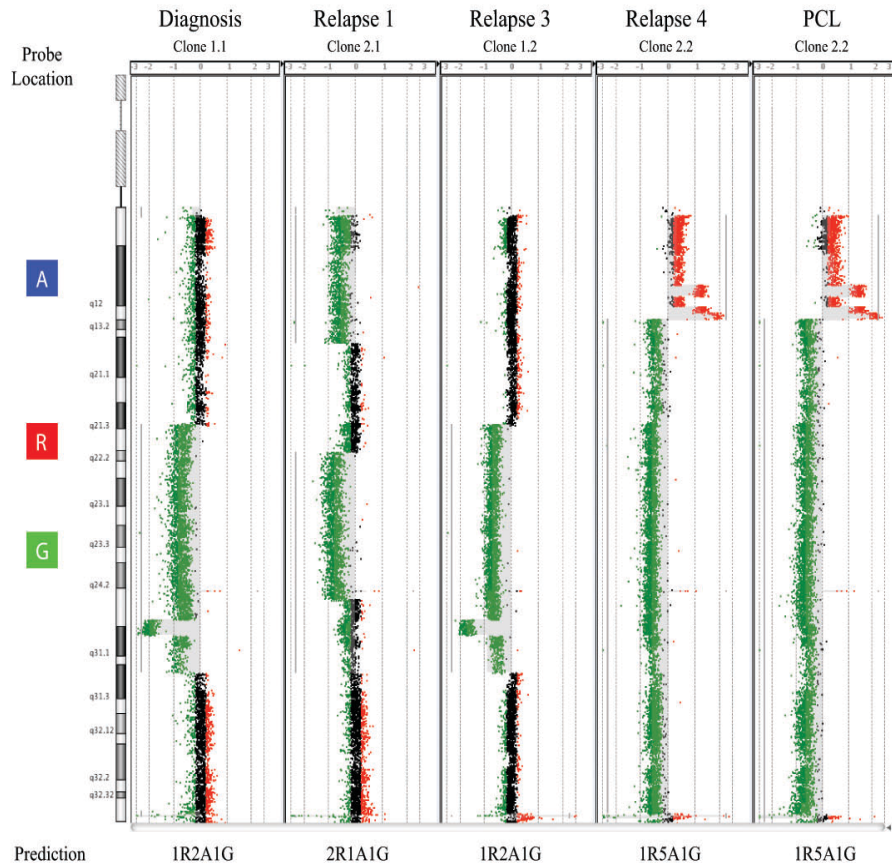Supplemental Figure 5 – Chromosome 14 (Progenitor 1 vs 2.1 vs 2.2)

A)

B)

Clone	Phenotype	Diag	Rem	R1	R2	R3	R4 -PC	R4 -LC	PCL-PC	PCL-LC
1.1, 1.2	1R2A1G	68%	91.9%	23.5%	54.2%	86%	97.1%			
Clone 2.1	2R2A1G	20%	8.1%	4.3%	18.6%	13%				
	2R1A1G			71.7%	20.3					
Clone 2.2	2R5A2G						2.9%	16.7%	58.2%	34.8%
	2R6A2G							62.1%	29.9%	45.5%
	2R3A2G							15.2%	6.7%	
	2R4A2G							4.5%	1.5%	12.1%
Misc	2R2A2G	9%								
	1R1A1G	2%		0.5%	5.1%	1.0%				
	2R1A2G	1%								
	3R1A1G				1.7%					
	2R3A1G							1.5%		
	3R6A2G								3.7%	7.6%
Cells			100	37	187	59	100	34	66	134	66

A) The relative position of each FISH probe is shown beside the aCGH results. See Suppl Figure 2A.

B) The number of cells counted and the percentage of each phenotype shown by FISH. See Suppl Figure 2B.

Supplemental Figure 6 – Chromosome 11/BIRC (Progenitor 1 vs 2.1 vs 2.2)

A)

B)
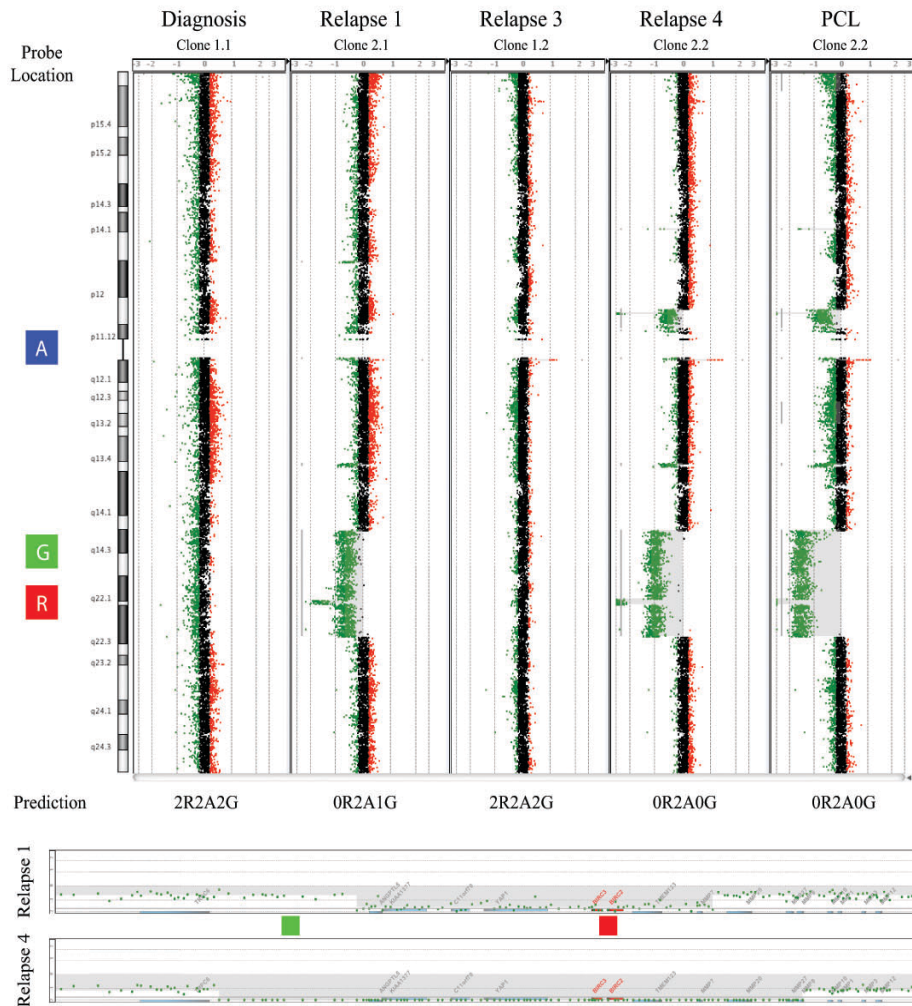
Clone	Phenotype	Diag	Rem	R1	R2	R3	R4 -PC	R4 -LC	PCL-PC	PCL-LC
Clone 1	2R2A2G	88%	93.3%	36%	60%	84%	86%		1.4%	
Clone 1	4R4G4A					8%				
Clone 2.1	0R2A1G	12%		49%	6%	4%				
Clone 2.2	0R2A0G			13%	28%	4%	4%	4%	5.4%	11.3%
Clone 2.2	0R3A0G						10%	88%	89.8%	75.5%
Clone 2.2	0R4A0G						8%	3.4%	13.2%	
Misc	2R1A2G		3.3%		6%					
Misc	0R1A0G		3.3%							
Misc	0R1A1G			2%						
Cells			50	30	100	50	50	50	50	53	147

A)   The relative position of each FISH probe is shown beside the aCGH results. See Suppl Figure 2A.

B)   The number of cells counted and the percentage of each phenotype shown by FISH. See Suppl Figure 2B.

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Supplemental Figure 7 – Chromosome 5 (Does 2.2 pre-exist?)

A)

B)
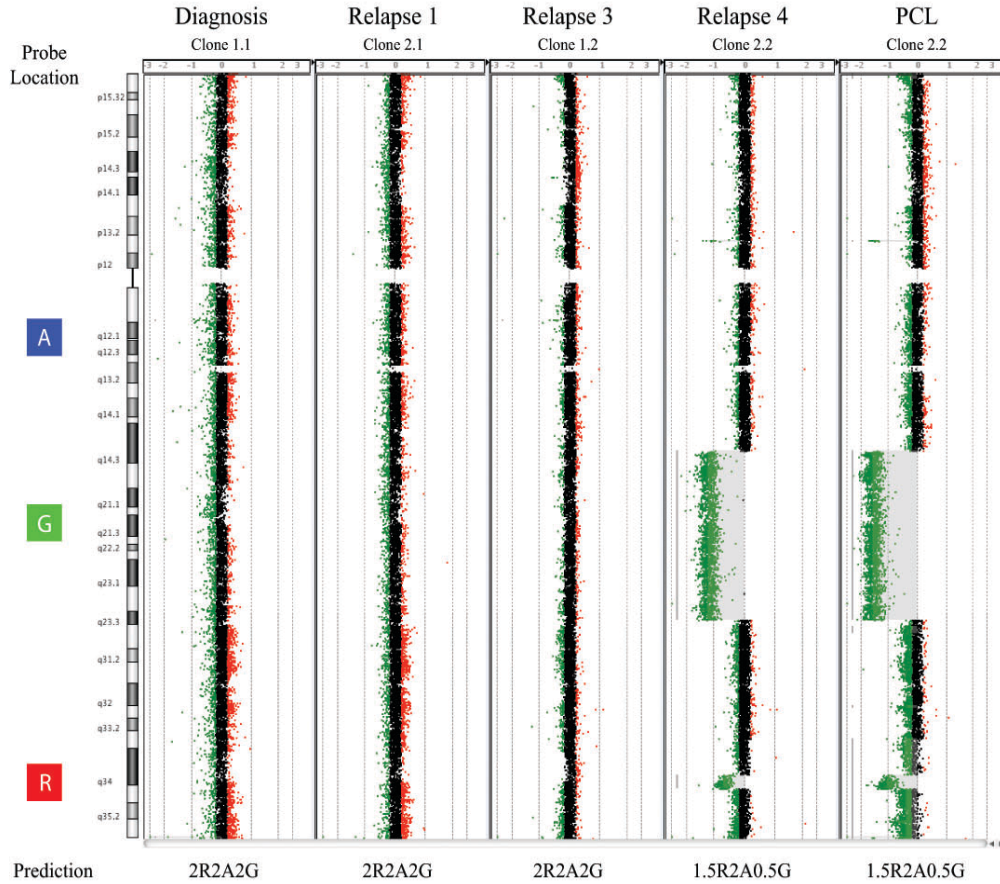
Clone	Phenotype	Diag	Rem	R1	R2	R3	R4 -PC	R4 -LC	PCL-PC	PCL-LC
1.1, 1.2, 2.1	2R2A2G	95%	90.9%	96.5%	92%	98%	100%			
	4R4A4G		6.1%		4%	1%				
Clone 2.2	2R2A1G	2%		0.5%				1.4%		
	1R2A1G			**0.5%**				**2.1%**	**1.6%**	**2.7%**
	1R2A2G			0.5%	1%					
	1R3A1G							6.8%	31.2%	33.3%
	2R3A1G							81.1%	67.2%	62.7%
	2R3A1G							1.4%		
	1R4A1G									1.3%
Misc	2R1A2G	3%	3%	1.5%	4%					
	2R1A1G			0.5%						
	1R3A2G							4.1%		
Cells		100	33	200	100	100	26	74	125	75

A) The relative position of each FISH probe is shown beside the aCGH results. See Suppl Figure 2A.

B) The number of cells counted and the percentage of each phenotype shown by FISH. See Suppl Figure 2B.

Supplemental Figure 8 – Chromosome 17 (Does 2.2 pre-exist?)
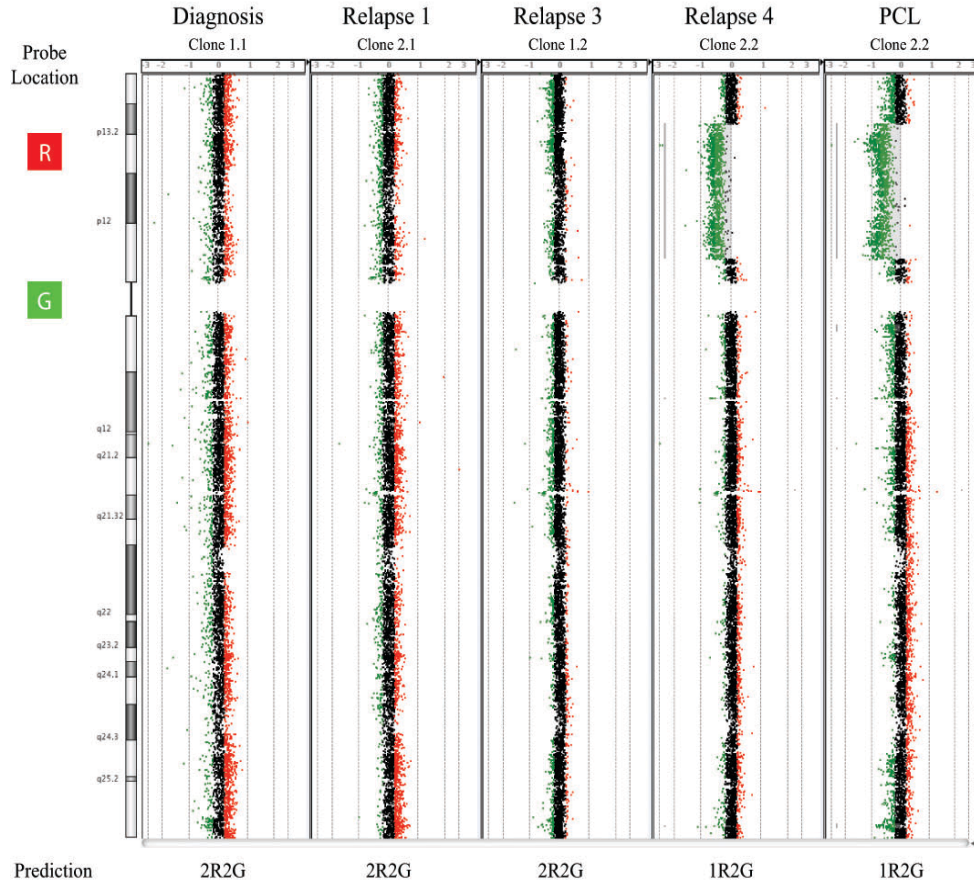
A)

	Diagnosis	Relapse 1	Relapse 3	Relapse 4	PCL
Prediction	2R2G	2R2G	2R2G	1R2G	1R2G

B)

Clone	Phenotype	Diag	Rem	R1	R2	R3	R4 -PC	R4 -LC	PCL-PC	PCL-LC
1.1, 1.2, 2.1	2R2G	86%	78.8%	70.7%	68%	64%	90.3%	10%	14.7%	24%
1.1, 1.2, 2.1	4R4G					4%				
Clone 2.2	1R2G	6%	3.0%	8.7%	16%	2%	9.7%			
Clone 2.2	2R3G							82%	84.7%	76%
Clone 2.2	2R4G							8%		
Misc	3R2G	6%				2%				
Misc	2R1G	2%	18.2%	9.3%	4%	26%				
Misc	1R1G			2.0%	8%					
Misc	3R3G				2%					
Misc	0R2G				2%					
Misc	4R3G					2%				
Misc	1R3G								0.6%	
Cells			50	33	150	50		62	50	50

A) The relative position of each FISH probe is shown beside the aCGH results. See Suppl Figure 2A.

B) The number of cells counted and the percentage of each phenotype shown by FISH. See Suppl Figure 2B.

Supplemental Figure 9 – Chromosome 20 (Does 2.2 pre-exist?)

A)

B)
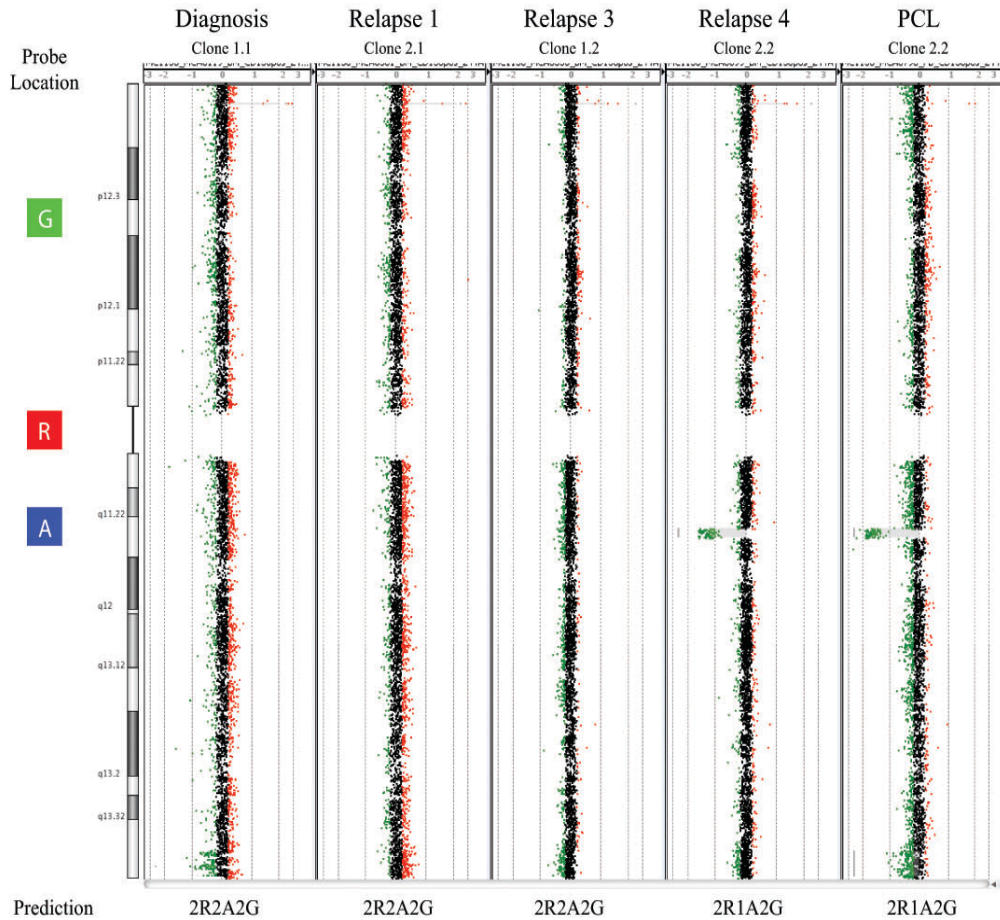
Clone	Phenotype	Diag	Rem	R1	R2	R3	R4 -PC	R4 -LC	PCL-PC	PCL-LC
1.1, 1.2, 2.1	2R2A2G	90.2%	96.7%	98.0%	87.1%	92%	90.0%			
	4R4A4G	7.8%			7.1%	2.0%	10.0%			
Clone 2.2	2R1A2G		3.3%		2%					
	3R1A3G*							95%	100%	100%
	4R1A4G*							2.5%		
Misc	1R2A2G	2.0%			2.9%	2%				
	2R2A1G			2.0%	2.9%					
	2R1A1G					2%				
	3R1A2G							2.5%		
Cells			51	30	100	70	50	10	40	52	48

A) The relative position of each FISH probe is shown beside the aCGH results. See Suppl Figure 2A.

B) The number of cells counted and the percentage of each phenotype shown by FISH. See Suppl Figure 2B.